# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/01 07:01:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472804.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3472804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472804.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Oct 01 07:01:28 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472804.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,190,198 |
| Mapped reads | 1,681,476 / 76.77% |
| Unmapped reads | 508,722 / 23.23% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 16,938 / 0.77% |
| Read min/max/mean length | 30 / 76 / 76.27 |
| Duplicated reads (estimated) | 86,006 / 3.93% |
| Duplication rate | 3.69% |
| Clipped reads | 1,025,508 / 46.82% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 27,955,735 / 26.58% |
| Number/percentage of C's | 21,091,071 / 20.05% |
| Number/percentage of T's | 30,961,110 / 29.44% |
| Number/percentage of G's | 25,158,026 / 23.92% |
| Number/percentage of N's | 2,123 / 0% |
| GC Percentage | 43.98% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.034 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2887 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.61 |

## 2.5. Mismatches and indels

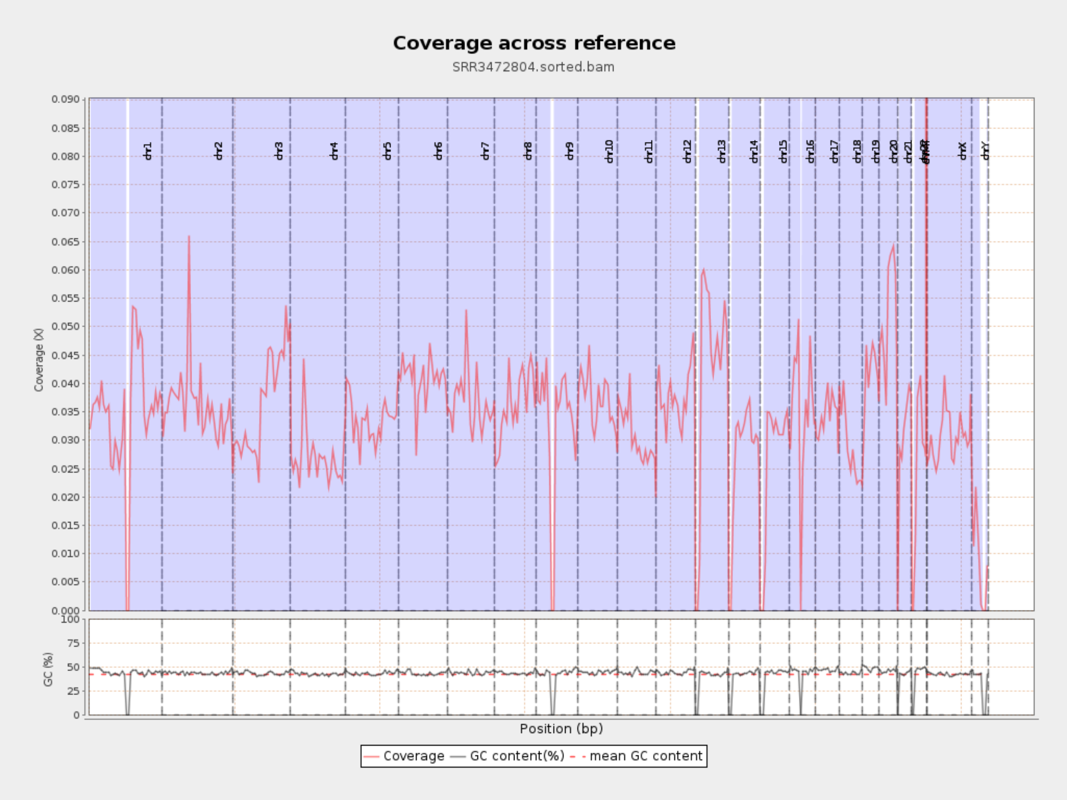
| | |
|---|---|
| General error rate | 0.91% |
| Mismatches | 940,488 |
| Insertions | 8,352 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 26,012 |
| Mapped reads with at least one deletion | 1.53% |
| Homopolymer indels | 45.27% |

## 2.6. Chromosome stats

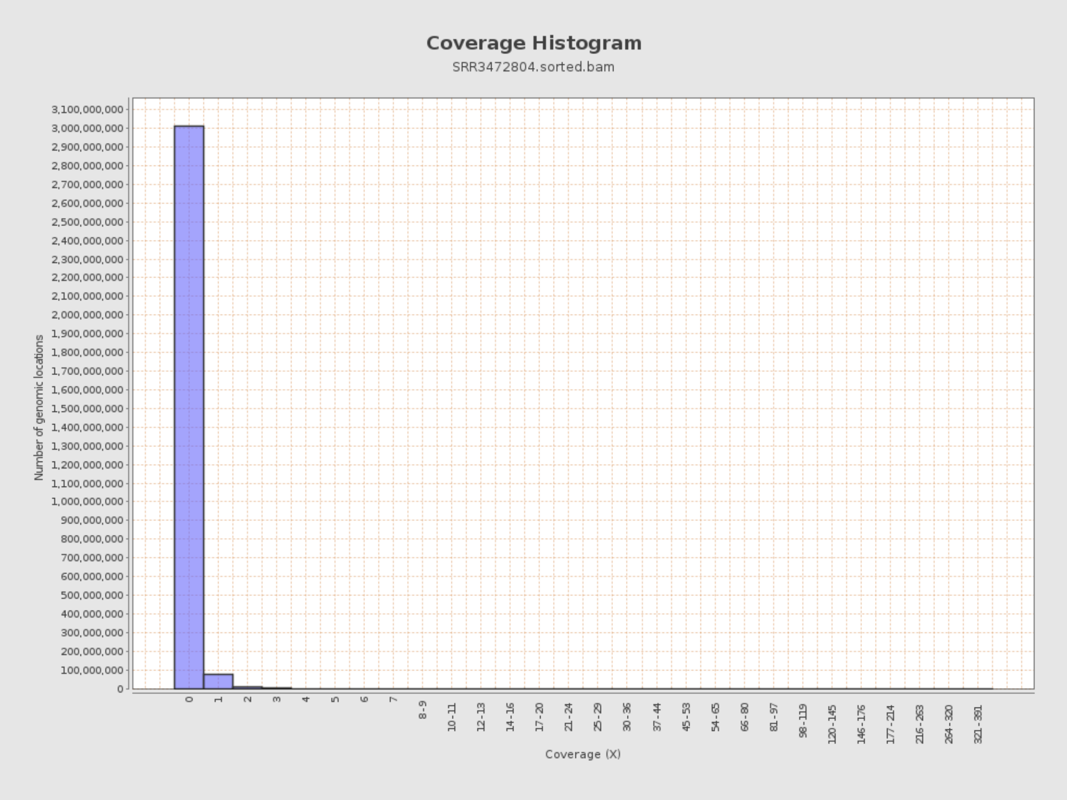
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8564298 | 0.0344 | 0.3453 |
| chr2 | 243199373 | 8865871 | 0.0365 | 0.375 |
| chr3 | 198022430 | 7177441 | 0.0362 | 0.2311 |
| chr4 | 191154276 | 5098943 | 0.0267 | 0.226 |
| chr5 | 180915260 | 6054829 | 0.0335 | 0.225 |
| chr6 | 171115067 | 7005344 | 0.0409 | 0.2643 |
| chr7 | 159138663 | 5845271 | 0.0367 | 0.3678 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5305518 | 0.0362 | 0.2761 |
| chr9 | 141213431 | 4591405 | 0.0325 | 0.3009 |
| chr10 | 135534747 | 5038950 | 0.0372 | 0.2869 |
| chr11 | 135006516 | 4133840 | 0.0306 | 0.3001 |
| chr12 | 133851895 | 5065743 | 0.0378 | 0.2518 |
| chr13 | 115169878 | 4846266 | 0.0421 | 0.2529 |
| chr14 | 107349540 | 2887543 | 0.0269 | 0.2371 |
| chr15 | 102531392 | 2709685 | 0.0264 | 0.2291 |
| chr16 | 90354753 | 3186524 | 0.0353 | 0.2508 |
| chr17 | 81195210 | 2790681 | 0.0344 | 0.2507 |
| chr18 | 78077248 | 2268636 | 0.0291 | 0.4786 |
| chr19 | 59128983 | 2436647 | 0.0412 | 0.311 |
| chr20 | 63025520 | 3326641 | 0.0528 | 0.2981 |
| chr21 | 48129895 | 1449298 | 0.0301 | 0.2346 |
| chr22 | 51304566 | 1210845 | 0.0236 | 0.1987 |
| chrMT | 16571 | 132394 | 7.9895 | 5.4467 |
| chrX | 155270560 | 4739065 | 0.0305 | 0.2427 |
| chrY | 59373566 | 483370 | 0.0081 | 0.1388 |

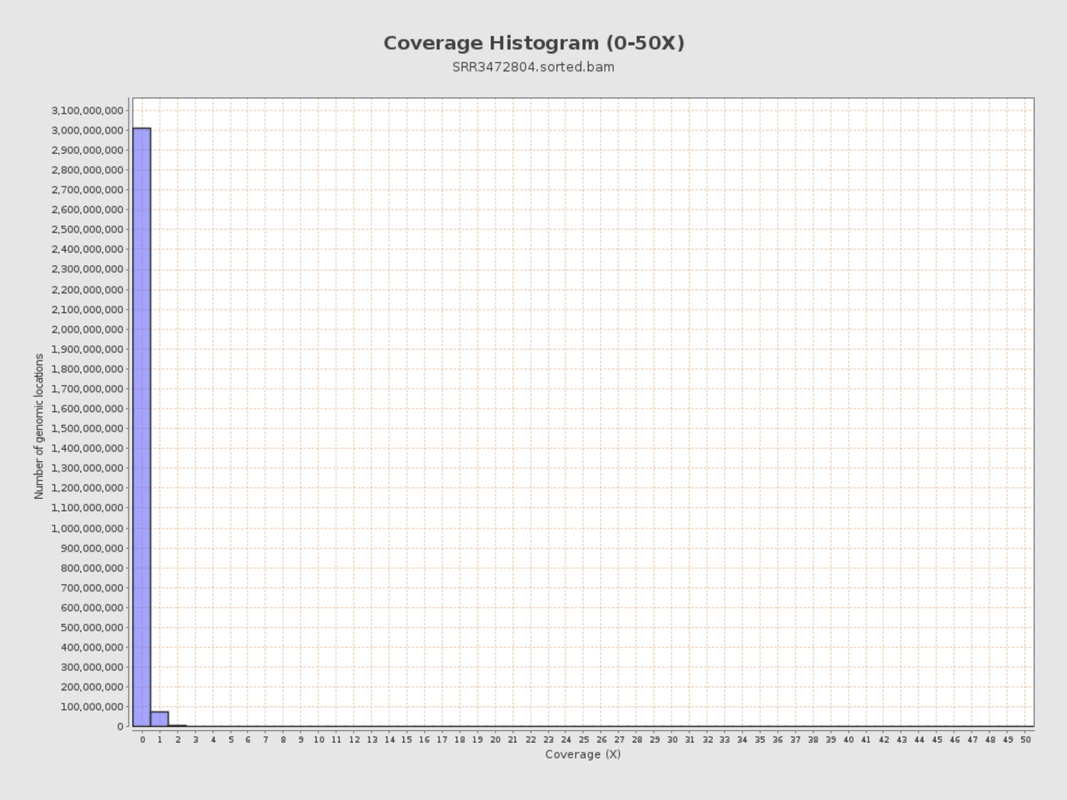
# 3. Results : Coverage across reference



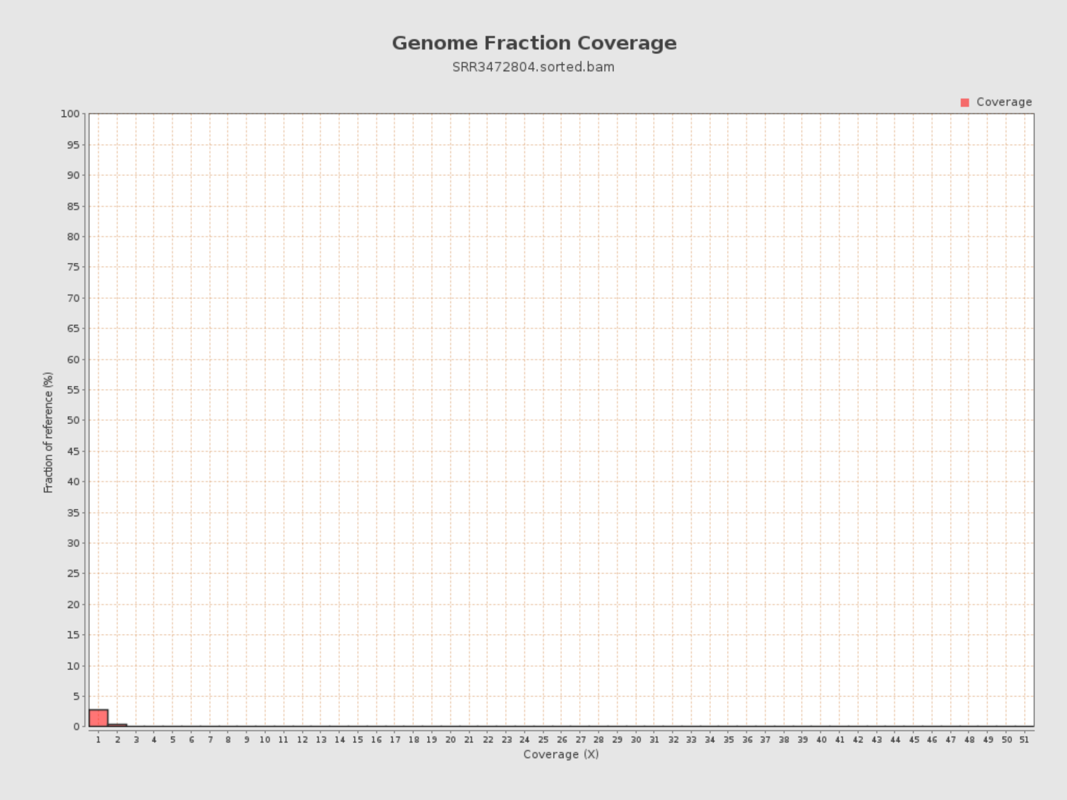
# 4. Results : Coverage Histogram



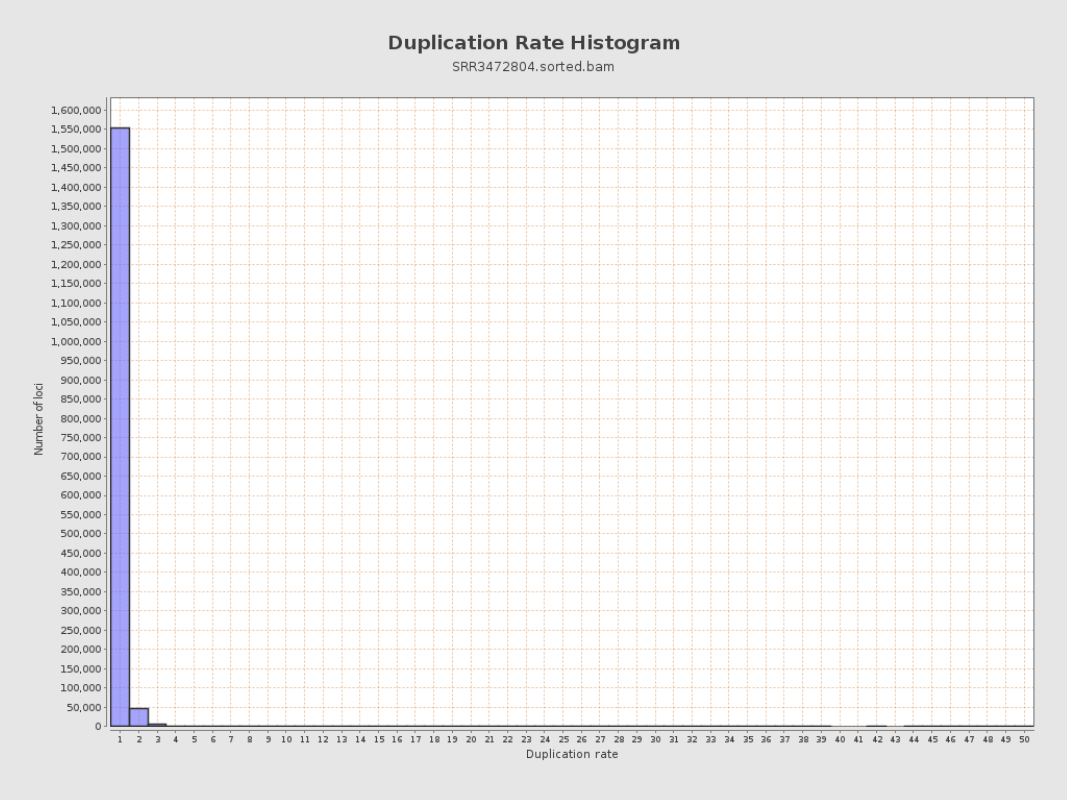
# 5. Results : Coverage Histogram (0-50X)



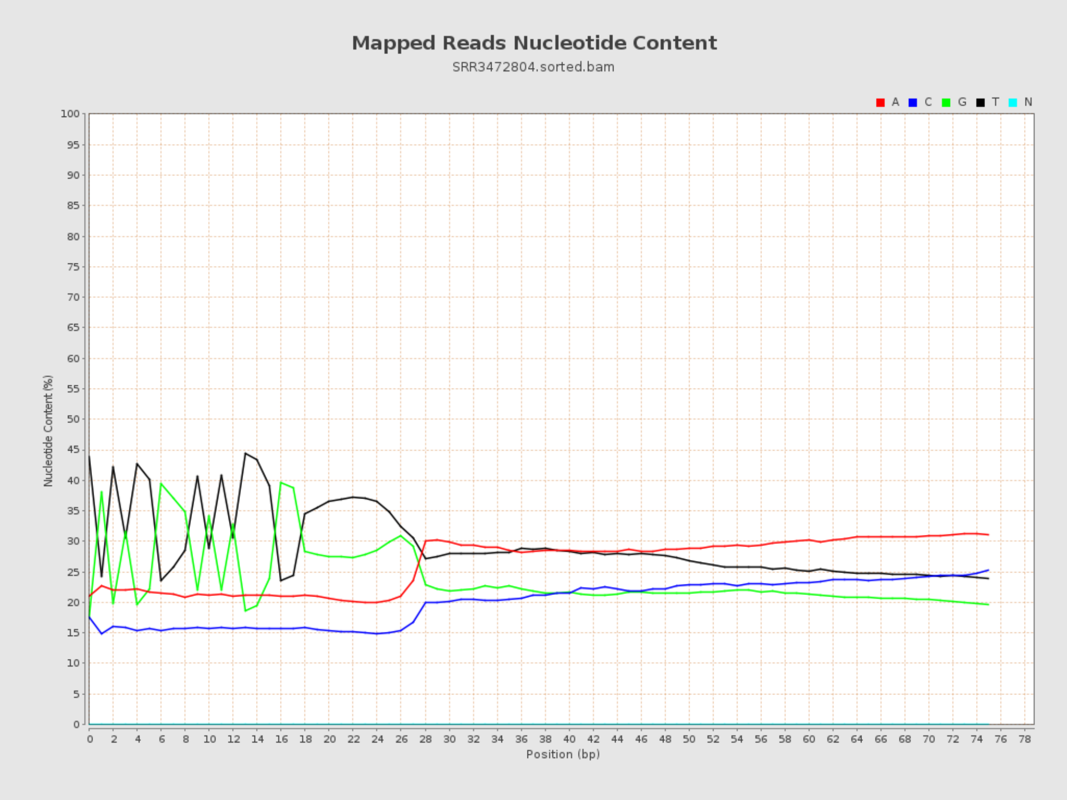
# 6. Results : Genome Fraction Coverage



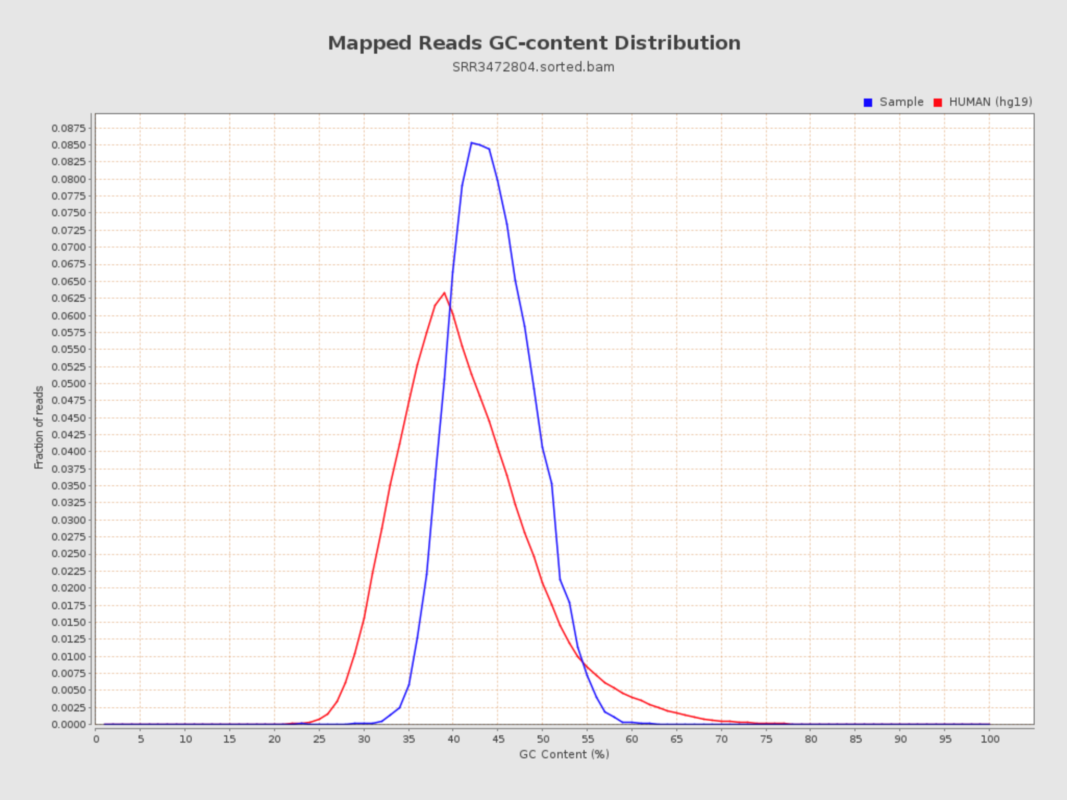
# 7. Results : Duplication Rate Histogram



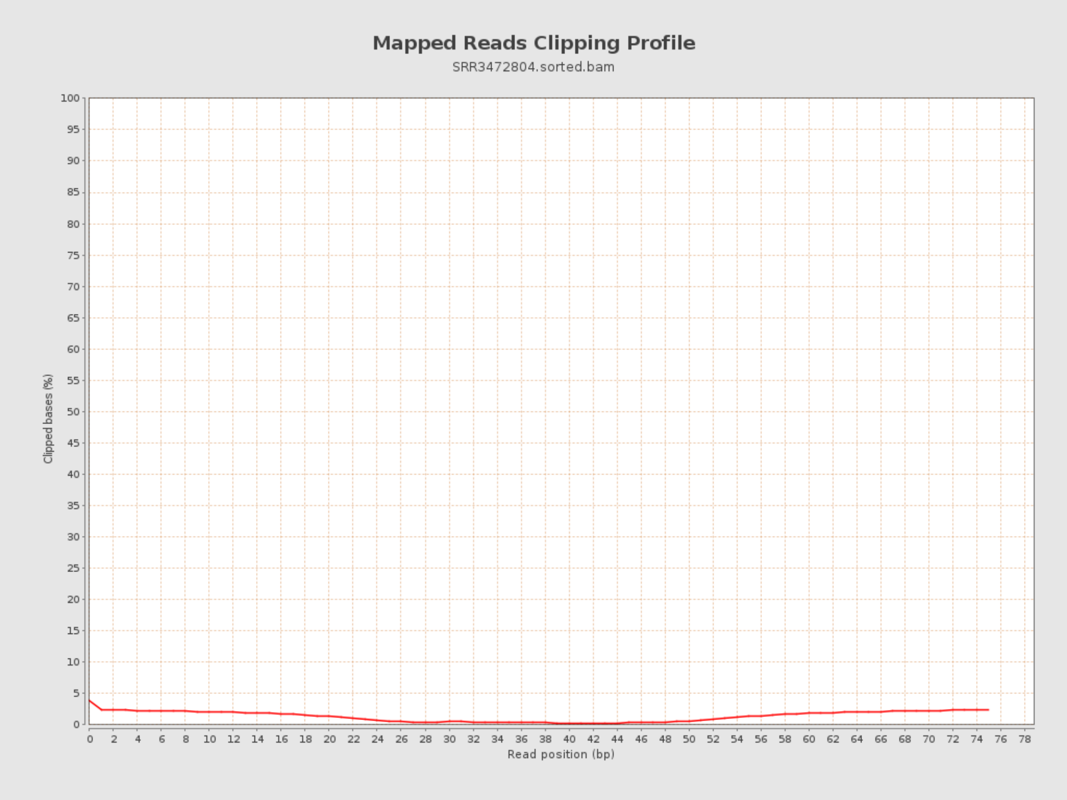
# 8. Results : Mapped Reads Nucleotide Content



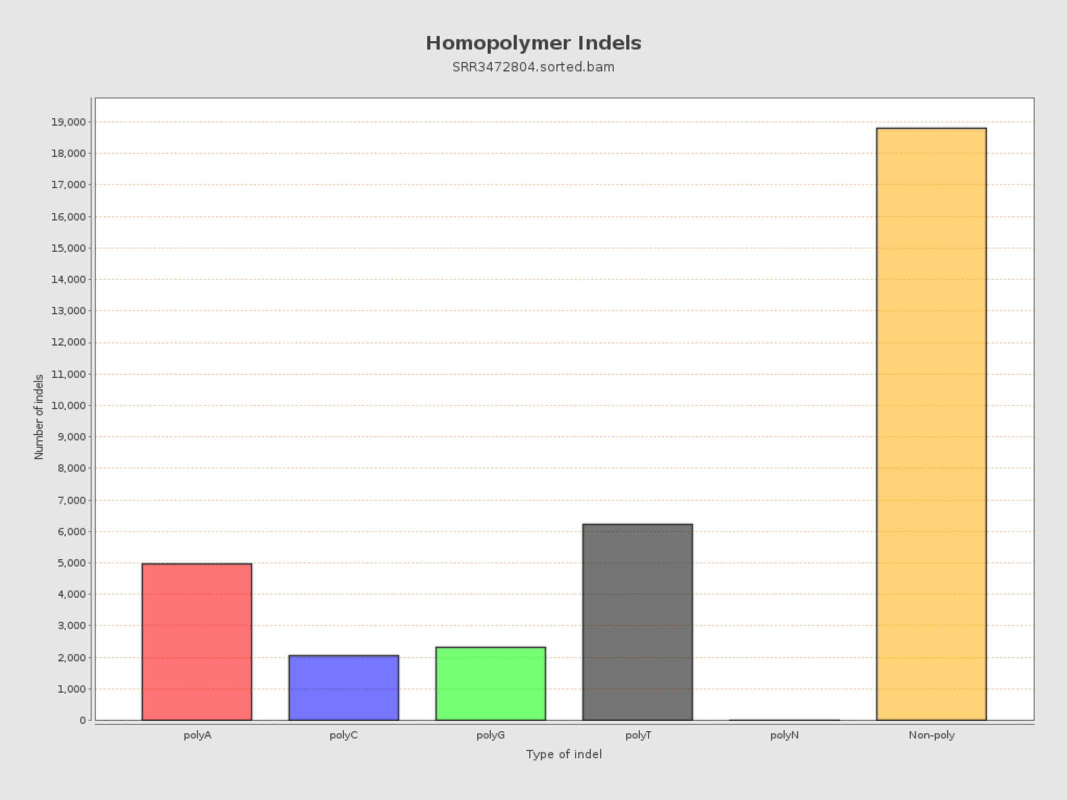
# 9. Results : Mapped Reads GC-content Distribution



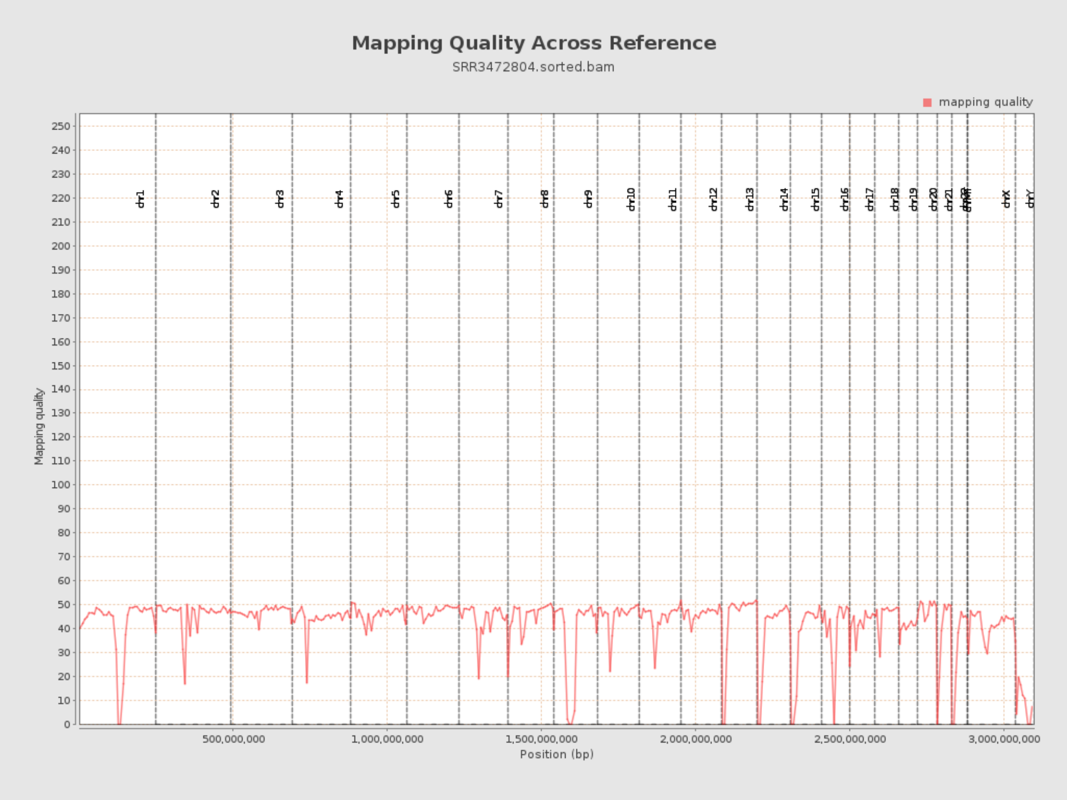
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram